

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:22:06 ; Search time 88.16 Seconds
(without alignments)
38.555 Million cell updates/sec

Title: US-09-331-631A-33

Perfect score: 77
Sequence: 1 CXXCXXCXXXXXXXXXXCXXCXXC 29

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTRMBL_15:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_unclassified:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	100.0	43	5	09VDN2
2	77	100.0	49	5	023947
3	77	100.0	49	5	023948
4	77	100.0	152	5	09XVX3
5	77	100.0	164	5	022048
6	77	100.0	188	5	018238
7	77	100.0	273	5	020000
8	77	100.0	314	5	023190
9	77	100.0	325	2	083828
10	77	100.0	625	10	09SP15
11	77	100.0	666	10	09SP14
12	77	100.0	666	10	09SP14
13	68	88.3	39	13	09PVG7
14	68	88.3	46	4	016861
15	68	88.3	62	10	065918
16	68	88.3	72	5	09V199
17	68	88.3	73	10	041615
18	68	88.3	74	5	09V1A1
19	68	88.3	75	5	096388

20	68	88.3	80	10	09SG42	09SG42 arabidopsis
21	68	88.3	83	11	09JM45	09JM45 mus muscu
22	68	88.3	84	13	090248	090248 bombyx bom
23	68	88.3	87	10	080641	080641 arabidopsis
24	68	88.3	89	11	088459	088459 mus muscu
25	68	88.3	91	10	049134	049134 fragaria an
26	68	88.3	97	10	038939	038939 arabidopsis
27	68	88.3	101	10	065313	065313 lavatera th
28	68	88.3	101	10	09XGJ3	09XGJ3 gerbera hyb
29	68	88.3	102	10	024040	024040 lavatera th
30	68	88.3	103	10	080848	080848 arabidopsis
31	68	88.3	106	10	049593	049593 arabidopsis
32	68	88.3	108	10	082328	082328 arabidopsis
33	68	88.3	110	6	09XSV4	09XSV4 canis fami
34	68	88.3	110	10	065066	065066 picea maria
35	68	88.3	112	10	043615	043615 petunia hyb
36	68	88.3	121	13	091450	091450 salvelinus
37	68	88.3	129	10	09LR14	09LR14 arabidopsis
38	68	88.3	136	2	09X8F4	09X8F4 streptomyce
39	68	88.3	169	4	014564	014564 homo sapien
40	68	88.3	177	10	09LIU5	09LIU5 oryza sativ
41	68	88.3	178	13	091AR5	091AR5 fuqua rubrip
42	68	88.3	191	6	028583	028583 ovis aries
43	68	88.3	191	6	09N0L8	09N0L8 macropus eu
44	68	88.3	230	11	064507	064507 mus muscu
45	68	88.3	242	5	019919	019919 caenorhabdi

ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	43	AA.
09VDN2	09VDN2	09VDN2	09VDN2	09VDN2	09VDN2
AC	09VDN2	09VDN2	09VDN2	09VDN2	09VDN2
DT	01-MAY-2000 (TREMBLrel. 13, Created)	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)	01-JUN-2000 (TREMBLrel. 14, Last annotation update)	01-JUN-2000 (TREMBLrel. 14, Last annotation update)	01-JUN-2000 (TREMBLrel. 14, Last annotation update)	01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE	CG5097 PROTEIN.	CG5097 PROTEIN.	CG5097 PROTEIN.	CG5097 PROTEIN.	CG5097 PROTEIN.
GN	CG5097	CG5097	CG5097	CG5097	CG5097
OS	Drosophila melanogaster (Fruit fly).	Drosophila melanogaster (Fruit fly).	Drosophila melanogaster (Fruit fly).	Drosophila melanogaster (Fruit fly).	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephydroidea; Drosophilidae; Drosophila.	Ephydroidea; Drosophilidae; Drosophila.	Ephydroidea; Drosophilidae; Drosophila.	Ephydroidea; Drosophilidae; Drosophila.	Ephydroidea; Drosophilidae; Drosophila.
OX	NCBI_TaxID=7227;	NCBI_TaxID=7227;	NCBI_TaxID=7227;	NCBI_TaxID=7227;	NCBI_TaxID=7227;
ON	111	111	111	111	111
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	STRAIN=BERKELEY;	STRAIN=BERKELEY;	STRAIN=BERKELEY;	STRAIN=BERKELEY;	STRAIN=BERKELEY;
RX	MEDLINE=20196006; PubMed=10731132;	MEDLINE=20196006; PubMed=10731132;	MEDLINE=20196006; PubMed=10731132;	MEDLINE=20196006; PubMed=10731132;	MEDLINE=20196006; PubMed=10731132;
RA	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA	Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,	Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,	Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,	Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,	Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA	Brandon R.C., Rogers Y.H.C., Blazey R.G., Champe M., Pfeiffer B.D.,	Brandon R.C., Rogers Y.H.C., Blazey R.G., Champe M., Pfeiffer B.D.,	Brandon R.C., Rogers Y.H.C., Blazey R.G., Champe M., Pfeiffer B.D.,	Brandon R.C., Rogers Y.H.C., Blazey R.G., Champe M., Pfeiffer B.D.,	Brandon R.C., Rogers Y.H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,
RA	Abriil J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,	Abriil J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,	Abriil J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,	Abriil J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,	Abriil J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA	Burley K.C., Busam D.A., Butler H., Cadlen E., Center A., Chandra I.,	Burley K.C., Busam D.A., Butler H., Cadlen E., Center A., Chandra I.,	Burley K.C., Busam D.A., Butler H., Cadlen E., Center A., Chandra I.,	Burley K.C., Busam D.A., Butler H., Cadlen E., Center A., Chandra I.,	Burley K.C., Busam D.A., Butler H., Cadlen E., Center A., Chandra I.,
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA	Dubin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,	Dubin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,	Dubin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,	Dubin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,	Dubin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA	Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,	Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,	Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,	Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,	Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA	Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,	Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,	Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,	Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,	Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA	Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,	Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,	Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,	Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,	Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA	Hoslin D., Houston K.A., Howland T.J., Wei M.-H., Ibeigwe C.,	Hoslin D., Houston K.A., Howland T.J., Wei M.-H., Ibeigwe C.,	Hoslin D., Houston K.A., Howland T.J., Wei M.-H., Ibeigwe C.,	Hoslin D., Houston K.A., Howland T.J., Wei M.-H., Ibeigwe C.,	Hoslin D., Houston K.A., Howland T.J., Wei M.-H., Ibeigwe C.,
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kethum K.A.,	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kethum K.A.,	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kethum K.A.,	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kethum K.A.,	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kethum K.A.,
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA	Liu X., Maitel B., McIntosh T.C., McLeod M.P., McPherson D.,	Liu X., Maitel B., McIntosh T.C., McLeod M.P., McPherson D.,	Liu X., Maitel B., McIntosh T.C., McLeod M.P., McPherson D.,	Liu X., Maitel B., McIntosh T.C., McLeod M.P., McPherson D.,	Liu X., Maitel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA	Merulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,	Merulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,	Merulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,	Merulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,	Merulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,


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RA Jones M., Kershaw J., Kirsten J., Laistler N., Latreille P.,
RA Lighting J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierly-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL NZ;
RA Leimbach D.;
RN Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RP [3]
RC SEQUENCE FROM N.A.
RC STRAIN-BRISTOL NZ;
RA Waterston R.;
RN Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RP [4]
RC SEQUENCE FROM N.A.
RC STRAIN-BRISTOL NZ;
RA Waterston R.;
RN Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U46675; AAB52645.1; -
SO SEQUENCE 273 AA; 29231 MW; 11542812CC566530 CRC64;

Query Match 100.0%; Score 77; DB 5; Length 273;
Best Local Similarity 20.7%, Pred. No. 20;
Matches 6; Conservative 23; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXCXGXXXXXXXXXXXXXGXGXXC 29
Db 214 CSTCTNCPSTCSQANCIPQCMPRLPTC 242
|::|::|::|::|::|::|::|::|::|::|

RESULT 8
ID Q23390 PRELIMINARY; FRT; 314 AA.
AC Q23390;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JAN-1999 (TREMBLrel. 09, Last annotation update)
DE ZK1067.7 PROTEIN.
GN ZK1067.7.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoides;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Thomas K.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jlier W., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
RA Shaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierly-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Nature 368:32-38(1994).
RX EMBL; Z70038; CAAG3886.1; -
SO SEQUENCE 314 AA; 32803 MW; 8735F50B826ED303 CRC64;
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Query Match Similarity      100.0%; Score 77; DB 5; Length 314;
Best Local Similarity      20.7%; Pred. No. 22;
Matches      6; Conservative 23; Mismatches      0; Indels      0; Gaps      0

Qy      1 CXXCXXCXXXXXXCXXXXXXCXXXXC 29
      1:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      105 CNGCQDCCISCACFPICACSNNGSSC 133

RESULT      9
O83828      PRELIMINARY;      PRT;      325 AA.
AC      O83828;
DT      01-NOV-1998 (TREMBLrel. 08. Created)
DT      01-NOV-1998 (TREMBLrel. 08. Last sequence update)
DE      01-MAY-2000 (TREMBLrel. 13. Last annotation update)
DE      HYPOHETICAL 34.1 KDA PROTEIN.
GN      TP0856.
OS      Treponema pallidum.
OC      Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX      NCBI_TaxID=160;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=NICHOLS;
RA      MEDLINE=98332770; PubMed=9665876;
RA      Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,
RA      Dodson R., Gwyn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA      Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA      Khelai H., Richardson D., Howell J.K., Childsbarrow M., Uitterback T.,
RA      McDonald L., Artlach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA      Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA      Venter J.C.;
RT      "Complete genome sequence of Treponema pallidum, the syphilis
RT      spirochete.";
RL      Science 281:375-388(1998).
DR      EMBL; AE001256; AAC65828.1; -.
DR      TIGR; TP0856; -.
KW      Hypothetical protein.
SQ      SEQUENCE      325 AA; 34054 MW; F9CFDCBD253C07D2 CRC64;

Query Match      100.0%; Score 77; DB 2; Length 325;
Best Local Similarity      20.7%; Pred. No. 22;
Matches      6; Conservative 23; Mismatches      0; Indels      0; Gaps      0;

Qy      1 CXXCXXCXXXXXXCXXXXXXCXXXXC 29
      1:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      238 CXTSGRCTGVGTCCNGERPKCKDCDCNC 266

RESULT      10
O9SPL3      PRELIMINARY;      PRT;      625 AA.
ID      O9SPL3;
AC      O9SPL3;
DT      01-MAY-2000 (TREMBLrel. 13. Created)
DT      01-MAY-2000 (TREMBLrel. 13. Last sequence update)
DT      01-OCT-2000 (TREMBLrel. 15. Last annotation update)
DE      VICILIN PRECURSOR (FRAGMENT).
GN      AMP2.
OS      Macadamia integrifolia (Macadamia nut).
OC      Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC      Magnoliophyta; Eudicotyledons; Proteaceae; Macadamia.
OX      NCBI_TaxID=60698;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=NUT KERNEL;
RA      Marcus J.P., Goulter K.C., Green J.L., Mannens J.M.;
RA      "A family of antimicrobial peptides is produced by processing of a 7S
RT      globulin protein in Macadamia integrifolia.";
RL      Plant J. 0:0-0(1999).
EMBL; AF161885; AAD54246.1; -.
HSSP; P02853; 2PHL.

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